

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 14, 2001, 02:37:58 ; Search time 52.5 seconds

(without alignments)
434.564 Million cell updates/sec

Title: US-09-481-990-2

Perfect score: 1753

Sequence: 1 MLOSLAGSSCVLRHRSRA.....QNEPFAVATQSSACVDGPANH 336

Scoring table:

Gapop 10.0 , Gapext 0.5

Archived: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR.66:*
2: pir2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1753	100.0	336	2	S65566 inward rectifier p
2	430.5	24.6	392	2	T45032 hypothetical prote
3	300	17.1	393	2	T25392 hypothetical prote
4	295	16.8	427	2	T27681 hypothetical prote
5	294.5	16.8	443	2	T21598 hypothetical prote
6	294	16.8	334	2	T19860 hypothetical prote
7	294	16.8	364	2	T43361 probable potassium
8	291	16.6	329	2	T43509 probable potassium
9	284.5	16.2	336	2	T33347 outward rectifier
10	264.5	15.1	1001	2	T13807 potassium channel
11	256.5	14.6	475	2	T27725 hypothetical prote
12	251	14.3	383	2	T23182 hypothetical prote
13	246	14.0	522	2	T24265 hypothetical prote
14	244	13.9	631	2	T26232 hypothetical prote
15	244	13.7	513	2	T28933 hypothetical prote
16	240	13.7	539	2	T23700 hypothetical prote
17	236	13.5	528	2	T21834 hypothetical prote
18	231	13.2	523	2	T23373 hypothetical prote
19	226.5	12.9	383	2	T23746 hypothetical prote
20	222.5	12.7	335	2	S44635 f2237.7 protein -
21	222	12.7	524	2	T23907 hypothetical prote
22	222	12.7	1539	2	T30037 hypothetical prote
23	219.5	12.5	700	2	T27364 hypothetical prote
24	213.5	12.2	485	2	T24201 hypothetical prote
25	211.5	12.1	769	2	T27550 hypothetical prote
26	209.5	12.0	660	2	T21551 hypothetical prote
27	209	11.9	452	2	T21118 hypothetical prote
28	204	11.6	544	2	T43364 potassium channel
29	204	11.6	576	2	T43363 potassium channel

30	204	11.6	643	2	T26616 hypothetical prote
31	199.5	11.4	1136	2	T26953 hypothetical prote
32	199	11.4	681	2	T19429 hypothetical prote
33	194.5	11.1	405	2	T21188 hypothetical prote
34	192	11.0	569	2	T43531 probable potassium
35	192	11.0	600	2	T24626 hypothetical prote
36	190.5	10.9	325	2	T15584 hypothetical prote
37	190.5	10.9	484	2	T43529 probable potassium
38	190.5	10.9	519	2	T16629 hypothetical prote
39	190	10.8	504	2	T22289 hypothetical prote
40	189	10.8	550	2	T22557 hypothetical prote
41	188.5	10.8	551	2	T16426 hypothetical prote
42	188.5	10.8	555	2	T43357 potassium channel
43	187	10.7	381	2	T43393 potassium channel
44	183.5	10.5	586	2	T21683 hypothetical prote
45	180.5	10.3	461	2	T43394 potassium channel

ALIGNMENTS

```

RESULT
1
S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65566
R:Lesage, F.; Guillemaire, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanl
Embo J. 15, 1004-1011, 1996
A>Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove
A:Reference number: S65566; MUID:96183184
A:Accession: S65566
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U033632; NID:g1086490; PIDD:AAB01688.1; PID:g1086491

Query Match      100.0%; Score 1753; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOSLAGSSCVLRHRSRAACGFGVLGYLLVFGAVVSSVELPREDLLRQELRLK 60
    |||||||
DB 1 MLOSLAGSSCVLRHRSRAACGFGVLGYLLVFGAVVSSVELPREDLLRQELRLK 60

QY 61 RRFLEHECLSEOOLEDFLGRVLEASNYGVSVLSNAGNMNMDFTSALFFASTVLTSTGY 120
    |||||||
DB 61 RRFLEHECLSEOOLEDFLGRVLEASNYGVSVLSNAGNMNMDFTSALFFASTVLTSTGY 120

QY 121 GHVPLSLDGGKAFCIIVSVIGIPFTLLFLNAVORITVHTRRPVLYPHIRMGFSKQYVA 180
    |||||||
DB 121 GHVPLSLDGGKAFCIIVSVIGIPFTLLFLNAVORITVHTRRPVLYPHIRMGFSKQYVA 180

QY 181 IVHAVILGFVTVSGFFPRPAVEFVLEDDNMFLSFYCFSTLSITGIGDVPVPGGYNOK 240
    |||||||
DB 181 IVHAVILGFVTVSGFFPRPAVEFVLEDDNMFLSFYCFSTLSITGIGDVPVPGGYNOK 240

QY 241 FRELXKIGITCYLLGLTAMLVLETFCLELKKFRKMFYVKDKDDQVHIIEHDLS 300
    |||||||
DB 241 FRELXKIGITCYLLGLTAMLVLETFCLELKKFRKMFYVKDKDDQVHIIEHDLS 300

QY 301 FSSITDQAAGKEDQKONEPFAVATQSSACVDGPANH 336
    |||||||
DB 301 FSSITDQAAGKEDQKONEPFAVATQSSACVDGPANH 336

RESULT
2
T45032
hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032

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Db 393 LRKKEVKK 401

RESULT 5

T21598

hypothetical protein F31d4.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21598

R:Mortimore, B.

submitted to the EMBL Data Library, March 1997

A:Reference number: 219447

A:Accession: T21598

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-443 <WILD>

A:Cross-references: EMBL:292832; PIDN:CA07375.1; GSPDB:GN00023; CESP:F31d4.7

A:Experimental source: clone F31d4

C:Genetics:

A:Gene: CESP:F31d4.7

A:Map position: 5

A:introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 16.8%; Score 294.5; DB 2; Length 443;

Best Local Similarity 26.3%; Pred. No. 3.3e-18;

Matches 94; Conservative 63; Mismatches 124; Indels 77; Gaps 12;

QY 26 LVLGVLTVGVAVFSSVELPYEDLLRQELRKRRFLEEHCLSEQOLEOFLGRVLEA 85

DB 17 LIIIVFLVLCISGGLVFWLIEEPYQ---SELRDAMQHKIEENN---TARDAMMKKIFEN 69

QY 86 SNYGVSVLSNAGS-----NW-----NWDTSALFASVLSSTTGYG 121

DB 70 SOLYLIRKNTSQRLLTFPIELSGYENOLGVGWSOOKMDWDMNVLFFAGITCTTGGY 129

QY 122 HNVPLSDGKACIIISVIGIPETLLFLAVVQRITVH-----RRPVLFIHMGFS 175

DB 130 HLYPMTDARMLTMTFALGILMLLVLDLFGALLITTMKFPFQTKR--LMRRIMRCT 187

QY 176 KQVVALVNAV-----LLGFVVSCEFPIPAVFSVLEDDMNFLESFEYCF 220

DB 188 KQPIEMKRIEQRERHDLIDPLPLPVGIALIVTWIFICFVLSVMDHNTLLESFEYFF 247

QY 221 ISLSTIGLGDYVPEGYGNOKFRELKIGITC--YLLGLIAMLVLETCELHELKFRK 278

DB 248 TSLSTVGLDVLVPSSP-----RLITMFGFIIVLGLSVSMVINTL-----LQAKMK 292

QY 279 MRYVKKDKEDQVHILEHDQLSFSSTTDOAGMKEDOK---QNEPVTATOSSACVDG 332

DB 293 STYENGRNDEKTPHT--HOTLPTSLGVLCFSPDEERKTDYSERSUSRSYOTSLSLPG 348

RESULT 6

T19860

hypothetical protein C40C9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19860

R:Hemby, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: 219188

A:Accession: T19860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <WILD>

A:Cross-references: EMBL:270266; PIDN:CA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.1

A:Map position: X

A:introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 16.8%; Score 294; DB 2; Length 334;

Best Local Similarity 29.2%; Pred. No. 2.6e-18;

Matches 71; Conservative 56; Mismatches 88; Indels 28; Gaps 11;

QY 26 LVLGVLTVGVAVFSSVELPYEDLLRQELRKRRFLEEHCLSEQOLEOFLGRVLEA 85

DB 14 LIIITFTYLLFGAVFDKLESEKDIWDEITERIDRLKHKN--FSEKDLHLF-----EA 67

QY 86 SNYGVSVLSNAGSWMNMDFTSALFFASTVLSSTTGYGHTVPLSDGKACIIISVIGIPT 145

DB 68 --IAIKSIPQAG--YQMGFAGAFYFAIVITTVYGSHGAPSTNAGKLCMFALGVPMG 124

QY 146 LLFLTAVQRTIVYTR-----RPVLYFIHMGFS--KQVVALVNAV-----LGFVTVSCF 195

DB 125 LIMFOSIGERYNTFIAYSLHAFRSLH--OQGFYCLQDEVPTHLIWSLTIGFVAVISG 181

QY 196 FFIPAAVFSVLEDDMNFLESFECFISLSTIGLGDYVGEQYNO--KPRELYKIGITCYL 254

DB 182 TY-----MHHTIE--KMSIDAIYFCMTITSTIGFGDLVPLQOVNALDQPLVYFATIMFL 236

QY 255 LGL 257

DB 237 IGL 239

RESULT 7

T43361

probable potassium channel chain n2P20 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T43361

R:Wang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: 222450

A:Accession: T43361

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-364 <MAN>

A:Cross-references: EMBL:AF083646; PIDN:AAC32857.1

Query Match 16.8%; Score 294; DB 2; Length 364;

Best Local Similarity 29.2%; Pred. No. 2.9e-18;

Matches 71; Conservative 56; Mismatches 88; Indels 28; Gaps 11;

QY 26 LVLGVLTVGVAVFSSVELPYEDLLRQELRKRRFLEEHCLSEQOLEOFLGRVLEA 85

DB 14 LIIITFTYLLFGAVFDKLESEKDIWDEITERIDRLKHKN--FSEKDLHLF-----EA 67

QY 86 SNYGVSVLSNAGSWMNMDFTSALFFASTVLSSTTGYGHTVPLSDGKACIIISVIGIPT 145

DB 68 --IAIKSIPQAG--YQMGFAGAFYFAIVITTVYGSHGAPSTNAGKLCMFALGVPMG 124

QY 146 LLFLTAVQRTIVYTR-----RPVLYFIHMGFS--KQVVALVNAV-----LGFVTVSCF 195

DB 125 LIMFOSIGERYNTFIAYSLHAFRSLH--OQGFYCLQDEVPTHLIWSLTIGFVAVISG 181

QY 196 FFIPAAVFSVLEDDMNFLESFECFISLSTIGLGDYVGEQYNO--KPRELYKIGITCYL 254

DB 182 TY-----MHHTIE--KMSIDAIYFCMTITSTIGFGDLVPLQOVNALDQPLVYFATIMFL 236

QY 255 LGL 257

DB 237 IGL 239

RESULT 8

T43509

probable potassium channel chain n2P38 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43509
 R:Wang, Z.W.; Saikoff, L.
 submitted to the EMBL Data Library, August 1998
 A:Description: Potassium channels in *C. elegans*.
 A:Reference number: Z22450
 A:Accession: T43509
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-329 <WNA>
 A:Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match
 Best Local Similarity 16.6%; Score 291; DB 2; Length 329;
 Matches 80; Conservative 59; Mismatches 106; Indels 30; Gaps 10;

26 LVLYGLTVLVFGAVFSSVELPYEDLLRQELKRLFLHEHCISEQOLEQFLGRVLEA 85
 11 LIVCTLTLYLVGAVFDALEFENELRQKLVORREKLTKN-MSNADYE-----ILEA 64
 86 SNVGVSVLSNAGNNMDFTSALFPASTVLTSTGYGTVPLSDGKACITIVIGIPET 145
 65 TI--VKSPVHAG-YQWKFSGAFYFATVITTTIGHSTPMTDAGKVCMLYALAGIPLG 121
 146 LFLFAVQRTVHTVRPVLVYHIRMGSKOVAIVHVLGFTV--VSCFFPIPAVF 203
 122 LIMFOSIGERNMTFAK---LIRIRRAAGKQPI-VTSSDLIFCTGWMGILIFGAFMF 177
 204 SVLEDDNMFLESEYFCFISLTIGLDYVPEGYNQKRELYKIGTC---YLLGLIA 259
 178 SSVY-NMTYFPAVYVCFTVLTITIGFDYV-----ALQKRGSLQTOPEYFSLVF 226
 260 MLVVLEFCEHLEKFKRKFMYVKKDKEDQVHTI 294
 227 ILFGLTVISAMNLLVIRFLMTNTERDERDEQEI 261

RESULT 9
 T32347
 outward rectifier potassium channel homolog twk-23 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32347
 R:Murphy, J.; Mohlmann, P.; O'Neal, D.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of *C. elegans* cosmid F34D6.
 A:Reference number: Z21153
 A:Accession: T32347
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <NUP>
 A:Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
 A:Experimental source: strain Bristol N2; clone F34D6
 A:Gene: twk-23; CESP:F34D6.3
 A:Map position: 2
 A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match
 Best Local Similarity 16.2%; Score 284.5; DB 2; Length 336;
 Matches 85; Conservative 54; Mismatches 107; Indels 35; Gaps 11;
 26 LVLYGLTVLVFGAVFSSVELPYEDLLRQELKRLFLHEHCISEQOLEQFL 79
 11 LIVCTLTLYLVGAVFDALEFENELRQKLVORREKLTKN-MSNADYE-----ILEA 67
 80 GRVLEASNYGVSVLSNAGNNMDFTSALFPASTVLTSTGYGTVPLSDGKACITIVIGIPET 139
 68 --ILEART--VKSPVHAG-YQWKFSGAFYFATVITTTIGHSTPMTDAGKVCMLYAL 122
 140 IGIPFTLFLFAVQRTVHTVRPVLVYHIRMGSKOVAIVHVLGFTV--VSCFFPI 197

DB 123 ACIPILIMFOSIGERNMTFAK---LIRIRRAAGKQPI-VTSSDLIFCTGWMGILIP 178
 QY 198 IPAVFSVLEDDNMFLESEYFCFISLTIGLDYVPEGYNQKRELYKIGTC---YL 253
 DB 179 GCAFMSSEYE-NMTYFPAVYVCFTVLTITIGFDYV-----ALQKRGSLQTOPEYV 227
 QY 254 LLGLIAMLVLETCEHLEKFKRKFMYVKKDKEDQVHTI 294
 DB 228 FFLSVLFLFGLTVISAMNLLVIRFLMTNTERDERDEQEI 268

RESULT 10
 T13807
 potassium channel protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
 C:Accession: T13807
 R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
 Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
 A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from *D. melanogaster*
 A:Reference number: Z17770; MUID:97073152
 A:Accession: T13807
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1001 <GOL>
 A:Cross-references: EMBL:U55321; NID:93808067; PID:93808068; PIDN:AAC69250.1
 C:Genetics:
 A:Gene: ORK1
 A:Map position: 1

Query Match
 Best Local Similarity 15.1%; Score 264.5; DB 2; Length 1001;
 Matches 77; Conservative 51; Mismatches 106; Indels 29; Gaps 9;
 26 LVLYGLTVLVFGAVFSSVELPYEDLLRQELKRLFLHEHCISEQOLEQFLGR 81
 DB 9 LLIFISTIMFGAIVYHIEGEEKISRABQKQAINVYLLEIDGKNVTTQDEILDR 68
 QY 82 VLEASNYGVSVLSNAGNNMDFTSALFPASTVLTSTGYGTVPLSDGKACITIVIGIPET 140
 DB 69 ISDYCDKRPVLPYDPTPTWTFYHAFYFCSTVIGNISPTEGRRMIMAVSYI 128
 QY 141 GIPT-LLE-----LFAVQRTVHTVRPVLVYHIRMGSKOVAIVHVLGFTV 189
 DB 129 GIPVNGILFAGLGEYGRFEATYRRKRYKMTDMHYVPQGL--ITVVALIRG- 184
 QY 190 VVSCFFPIPAVFSVLEDDNMFLESEYFCFISLTIGLDYVPEGYNQKRELYKIGTC---YL 244
 DB 185 --IALFLLFSWVFYFE-NMPSISLAYSIVTTTIGFDYVPTFGANQREFGFWV 241
 QY 245 YKIGICYLLGLIAMLVLETCEHLEKFKRKFMYVKKDKEDQVHTI 294
 DB 242 YQIFVIVWTFISL-GYLVIMTF 263

RESULT 11
 T27725
 hypothetical protein ZK1251.8 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27725
 R:McMurray, A.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z20411
 A:Accession: T27725
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-475 <WIL>
 A:Cross-references: EMBL:Z68222; PIDN:CAA92504.1; GSPDB:GN00022; CESP:ZK1251.8
 A:Experimental source: clone ZK1251
 C:Genetics:
 A:Gene: CESP:ZK1251.8

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Oy 77 QFLGHTLEASNYGVSVLNSASGMMNMDFTSALFPASTVLTGTGHTVPLSDGGKACII 136
    : : : : | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 EWVRPISDGAISG--LINSRS--RFDHLSGLSFFSATVISTIGGTSTPRTLGRFTIV 155

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Hypothetical protein W06D1.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T26232
 R: Basham, V.
 submitted to the EMBL Data Library, November 1996
 A/Reference number: 220177
 A/Accession: T26232
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-631 <M1>
 A/Cross-references: EMBL:Z82073; PIDN:CA804926.1; GSPDB:GN00023; CESP:W06D12.5
 A/Experimental source: clone W06D12
 C/Genetics:
 A/Gene: CESP:W06D12.5
 A/Map position: 5
 A/Introns: 4/3; 50/1; 89/2; 153/1; 244/3; 285/3; 333/1; 384/2; 509/1; 553/3

Query Match 14.0%; Score 245; DB 2; Length 631;
 Best Local Similarity 26.0%; Pred. No. 1.1e-13;
 Matches 99; Conservative 52; Mismatches 130; Indels 100; Gaps 16;

```

18 RSAMCGF-----LVGLILVVGAVVSSV-----LPEDELROELRK 58
200 KSMWFAFHKKQIGFHFSSVILVLYTLGAVFWVESRHEKAKTLDHVNNLEHLDR 259
QY 59 LKRRFEE---HECLSEQLLEQFLGRV-----LEASNYGVLS-NSGNNMDPTSA 107
Db 260 LAENITESVNNINTTTEEMKYYIREAYTELKLEGGYKSTYYLEADNMKMTFESA 319
QY 108 LFFASVYLTGTGHTVPSDGGKAFCLISVIGIPFTLLFLTAVVQRTVHVRPRVLY 167
Db 320 FFFSMNVYTTGTGSIAPSTLGOVAVCYGFVPTLVLRDGLQFLVHLTK---LY 376
QY 168 FHIRMGFSK-----QVAIVHAVLLGFVYSCFFETPAAVFSYLE 207
Db 377 AH---GIQKFRELNGKHHDEDEIISLPKACLLLASTLGACTIETIFY----- 423
QY 208 DDMNFI-----SEYFCISLTIGLDYVPE---GYNKKFRELKIGITC---ITC 251
Db 424 DELSGPEPTGDMFLCFEFSISLTIGLDIMPNNAIVGNKNRIYENKIKRPIISI 483
QY 252 YLLGL-1AMLVLEFCLEHKKRKKFYKKDKDEQVHIIHDQLSFSSTIDQAG 310
Db 484 IFFGMAVTKVNNRTFTAV-ENGIFGAPTLVENKLD-----AIVTRSSAS 528
QY 311 MKEDOKONEPYAVQSSACVD 331
Db 529 VKPEDRPSTPKV--ORALSD 547

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RESULT 15
 933

biochemical protein C52B9.6 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 R/Nelson, J.
 submitted to the EMBL Data Library, July 1996
 A/Description: The sequence of C. elegans cosmid C52B9.
 A/Reference number: Z20545
 A/Accession: T28933
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-513 <NE1>
 A/Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9.6
 A/Experimental source: strain Bristol NZ; clone C52B9
 C/Genetics:
 A/Gene: CESP:C52B9.6
 A/Map position: X
 A/Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3

Query Match 13.9%; Score 244; DB 2; Length 513;
 Best Local Similarity 22.8%; Pred. No. 1.1e-13;

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Matches 81; Conservative 64; Mismatches 95; Indels 116; Gaps 15;
QY 26 LVGLILVVGAVVSSVLEPDELROELRLKRRFLEHCLSEQLLEQFLGRVLEA 85
Db 65 LVILFLYLTAGAVLEFYLEAPKE---LESDNISR---EAFNAIQEFEDLVKMRQA 119
QY 86 -SNYGVSV--LSNAGSNMN--MDFTSALFPASTVYST-----TYGHTVP 125
Db 120 YRNOFTAKHLNKTREDELWTFPNSMEFAATVITIVQVKNRSGNRVFSRGYGNLVP 179
QY 126 LSDGKAFCLISVIGIPFTLLFLTAVVQRTVHVRPRVLYFHIRMGFSKQV----- 178
Db 180 ITVTGRVACIIFALIGIPILLVITADIGKFLSEPLS---YLKRSYR-GFKRLRQSKRI 235
QY 179 -----VAIVHAVLLGFVYSC 194
Db 236 TSQYRSQSRSRSSVWGSSKASMNLDHDSDESDSAGDELRIPVFVILVLAATAIG 295
QY 195 FFFTPAAVFSVLEDDW---NLESEYFCISLTIGLDYVPGEGYNKKFRELKIGITC 251
Db 296 FLF-----QSMHELEYEAFYFCFTIMATVGRGDIYPNE-----QVYVFTMA 338
QY 252 YLLGL1AMLVLEFC-ELHKKRKKFYKKDKEDQ-----VHIIH 296
Db 339 YIIFGL-----SLATMCIDLAGEYIRKIHVIGTKMEDAKGAVMTGLQAGEHLKH 389

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Search completed: February 14, 2001, 12:56:12
 Job time: 37094 sec

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